

SEQUENCE LISTING

<110> Degussa AG

<120> A process for producing L-amino acids using strains of the
Enterobacteriaceae family

<130> 020481 BT

<160> 4

<170> PatentIn version 3.1

<210> 1
<211> 32
<212> DNA
<213> Synthetic sequence

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<221> Primer
<222> (1)..(32)
<223> galP1

<400> 1
cacaatctag ataaaccata ttggagggca tc 32

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<222> (1)..(25)
<223> galP2

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gggaggaagc ttggggagat taatc 25

<210> 3
<211> 1446
<212> DNA
<213> Escherichia coli

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<221> DNA fragment
<222> (1)..(1446)
<223> PCR product

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<221> CDS

<222> (33)..(1427)

<223> galP coding region

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ggg cgg tca aac aag gca atg acg ttt ttc gtc tgc ttc ctt gcc gct	101
Gly Arg Ser Asn Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala	
10 15 20	
ctg gcg gga tta ctc ttt ggc ctg gat atc ggt gta att gct ggc gca	149
Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala	
25 30 35	
ctg ccg ttt att gca gat gaa ttc cag att act tcg cac acg caa gaa	197
Leu Pro Phe Ile Ala Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu	
40 45 50 55	
tgg gtc gta agc tcc atg atg ttc ggt gcg gca gtc ggt gcg gtg ggc	245
Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly	
60 65 70	
agc ggc tgg ctc tcc ttt aaa ctc ggg cgc aaa aag agc ctg atg atc	293
Ser Gly Trp Leu Ser Phe Lys Leu Gly Arg Lys Lys Ser Leu Met Ile	
75 80 85	
ggc gca att ttg ttt gtt gcc ggt tcg ctg ttc tct gcg gct gcg cca	341
Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Ala Pro	
90 95 100	
aac gtt gaa gta ctg att ctt tcc cgc gtt cta ctg ggg ctg gcg gtg	389
Asn Val Glu Val Leu Ile Leu Ser Arg Val Leu Leu Gly Leu Ala Val	
105 110 115	
ggt gtg gcc tct tat acc gca ccg ctg tac ctc tct gaa att gcg ccg	437
Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro	
120 125 130 135	
gaa aaa att cgt ggc agt atg atc tcg atg tat cag ttg atg atc act	485
Glu Lys Ile Arg Gly Ser Met Ile Ser Met Tyr Gln Leu Met Ile Thr	
140 145 150	
atc ggg atc ctc ggt gct tat ctt tct gat acc gcc ttc agc tac acc	533
Ile Gly Ile Leu Gly Ala Tyr Leu Ser Asp Thr Ala Phe Ser Tyr Thr	
155 160 165	
ggt gca tgg cgc tgg atg ctg ggt gtg att atc atc ccg gca att ttg	581
Gly Ala Trp Arg Trp Met Leu Gly Val Ile Ile Ile Pro Ala Ile Leu	
170 175 180	
ctg ctg att ggt gtc ttc ttc ctg cca gac agc cca cgt tgg ttt gcc	629
Leu Leu Ile Gly Val Phe Phe Leu Pro Asp Ser Pro Arg Trp Phe Ala	
185 190 195	
gcc aaa cgc cgt ttt gtt gat gcc gaa cgc gtg ctg cta cgc ctg cgt	677
Ala Lys Arg Arg Phe Val Asp Ala Glu Arg Val Leu Leu Arg Leu Arg	
200 205 210 215	

gac acc agc gcg gaa gcg aaa cgc gaa ctg gat gaa atc cgt gaa agt	725
Asp Thr Ser Ala Glu Ala Lys Arg Glu Leu Asp Glu Ile Arg Glu Ser	
220 225 230	
ttg cag gtt aaa cag agt ggc tgg gcg ctg ttt aaa gag aac agc aac	773
Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu Asn Ser Asn	
235 240 245	
ttc cgc cgc gcg gtg ttc ctt ggc gta ctg ttg cag gta atg cag caa	821
Phe Arg Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln	
250 255 260	
ttc acc ggg atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa	869
Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu	
265 270 275	
ctg gcg ggt tat acc aac act acc gag caa atg tgg ggg acc gtg att	917
Leu Ala Gly Tyr Thr Asn Thr Thr Glu Gln Met Trp Gly Thr Val Ile	
280 285 290 295	
gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt	965
Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val	
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gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg	1013
Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met	
315 320 325	
gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac	1061
Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His	
330 335 340	
tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att	1109
Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile	
345 350 355	
gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc	1157
Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser	
360 365 370 375	
gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act	1205
Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr	
380 385 390	
gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc	1253
Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr	
395 400 405	
atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct	1301
Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala	
410 415 420	
ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc	1349
Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr	
425 430 435	
aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt	1397
Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg	
440 445 450 455	
aaa ctg cgc gaa ata ggc gct cac gat taa tctccccaag cttcctccc	1446
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460	

<210> 4

<211> 464

<212> PRT

<213> Escherichia coli

<400> 4

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Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
 35 40 45

Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
 50 55 60

Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
 65 70 75 80

Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
 85 90 95

Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
 100 105 110

Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
 115 120 125

Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
 130 135 140

Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
 145 150 155 160

Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
 165 170 175

Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro
 180 185 190

Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
 195 200 205

Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
 210 215 220
 Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
 225 230 235 240
 Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
 245 250 255
 Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
 260 265 270
 Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
 275 280 285
 Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
 290 295 300
 Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
 305 310 315 320
 Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
 325 330 335
 Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
 340 345 350
 Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
 355 360 365
 Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
 370 375 380
 Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
 385 390 395 400
 Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
 405 410 415
 Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
 420 425 430
 Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu
 435 440 445
 Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
 450 455 460